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TCAAGACGA GTTATTTTCA GCTGCTgaCT GGAGACGGTG CAGCTCTGGA TACGAGAGCA TTTCACATAT GGAGCTGGAT ACAACACAC ACCGGGAGA CTTCAAGAGT TTCAGACTGA
 GGAGAAAC TTTCCCTTCT GCTGCTACTG CTGCTGCCG TGCTTTTGA AGTCCACTTC CTTCATGTT TTTTCTGCTT CACCTTCGCT GCTCCGGCTG TTCTCTTTGG
 TTCTATTGAG CGGCTGGCCA GAGGATGAGA CTTCCCAAC TCTCCTTTT TACCTGGCTT GGCTGAGCTT GGAATTCATC TGCACTGTGT TGGGTGCCCC TGACTTGGCC 32
 M R L P K L L T F L L W Y L A W L D L E F I C T V L G A P D L G
 CAGAGACCC AGGGTTCAG GCCAGGATTG GCCAAGCAG AGGCCCCCC CTTGCCCGGA AGTCTTTCAG GCCAGGGGT CACAGCTATG GTGGGGGGC CACCAATGCC 72
 Q R P Q G S R P G L A K A E A K E R P P L A R N V F R P G G H S Y G G A T N A
 ATGCTGAGG CACGGGAGG CACGGGAGG ACAGGAGCC TGACACAGCC CAGNAGGAT GAACCAAA AGTGTCCCC CAGACCGGG GGCCTGAAC CCAAGCCAGG ACACCTCC
 N A R A K G G T G Q T G G L T Q P K K D E P K K L P P R P G G P E P K P G H P P 112
 CAAACAGCC AGCTACAGC CCGGACTGT ACCCCAAAG GACAGCTTCC CGGAGGCAAG GCACCCCAA AAGCAGATC TGTCCCCAG TCTTCTGCTG TGAAGAGGC CAGGAGGCC
 Q T R Q A T A R T V T P K G Q L P G K A P P K A G S V P S S F L L K K A R E P 152
 GGGCCCCAC GAGAGCCAA GGAGCGTTT CCGCCACCC CCATCACACC CCAGAGTAC ATGCTCTGCTG TGTACAGAC GCTGTCCGAT GCTGACAGAA AGGAGGCAA CAGCAGCGT
 G P P R E P K E P F R P P P I T P H E Y M L S L Y R T L S D A D R K G G N S S V 192
 AATGTCAGG CTGACCTTGC CAACACCATC ACCAGCTTTA TTGACAAAG GCAAGTAC CAGAGTCCG TGCTACGAA GCAGAGTAC GTCTTTCACA TTACTGCCCT GGAGAAGGAT
 K L E A G L A N T I T S F I D K G Q D D R G P V V R K Q R Y V F D I S A L E K D 232
 GGCTGCTG GGCCGAGCT CGGATCTTG CGGAGAGC CTTGGACAC GGCACGCA CCGTCCCC CAGAGCGGG GTGCTCCAG CTCAAGCTGT CCAGTCCCC CAGCGGCCG
 G L G A E L R I L R K K P S D T A K P A V P R S R R A A Q L K L S S C P S G R 272
 CAGCGCGCG CCTTCTGGA TGTGGCTCC GTGCGAGGC TGAGCGATC TGCTGGAG GTGTTGACA TCTGGAAGCT CTTTGAAC TTTAAGAACT CGGCCAGCT GTGCTGGAG
 Q P A A L L D V R S V P G L D G S G W E V F D I W K L F R N F K N S A Q L C L E 312
 CTGCAACCT CGGACCGG CAGACCGTG GACCTCCGTG GCTGGGCTT CGACCGGCC GCGCGCAGG TCCACAGAA GGCCTGTTC CTGTGTGTTG GCGCACCAA GAAACGGGAC
 L E A W E R G R T V D L R G L G F D R A A R Q V H E K A L F L V F G R T K K R D 352
 CTGTTCTTTA ATGAGATTAA GGCCGCTCT GGCAGGAGG ATAGACGCT GTATGAGTAC CTGTTACGC AGCGCGGCA AGCGCGGCC CCATCGGCA CTTGCCAGGG CAAGGACCC
 L F F N E I K A R S G Q D D K T V Y E Y L F S Q R R K R R A P S A T R Q G K R P 392
 AGCAAGACC TTAAGGCTG CTGCACTCG AAGGCACTC ATGTCAACTT CAAGCACATG GCTTGGAG CACTGGAGT CCGACCCCTT GAGTACGAG CTTTCCACTG CGAGCGGCTG
 S K N L K A R C S R K A L H V N F K D M G W D D W I L A P L E Y E A F H C E G L 412
 TCGAGTTCC CATTGCTTC CACCTGGAG CCACGAATC ATGAGTCTAT CCAGACCTG ATGACTGCA TGGACCCCA GTCCACACA CCACCTGCT GTGTGCCCA CCGGCTGAGT
 C E F P L R S H L E P T N H A V I O T L M N S M D P E S T P P T C C V P T R L S 472
 CCATCAGCA TCTCTTCTAT TCACCTGCC AACACGTTG TGTATAACA GTATAGGAC ATGCTGTTG AGTCGTGAG CAGCAGTAG CAGCAGTAG CTTCTGCTT CTTGCTGCTG 501
 P I S I L F I D S A N N V V Y K Q Y E D M V V E S C G C R . (SEQ. ID NO.: 13)
 ACATCCCAAG AGCCCTTCC TCACCTCTG GAATCAGCA AGCTTGGCA GGAGCATCTA CACAGCTTG TGAAGGATT CAATAGCTT GCTGCTCTC TGAGTCTGAC
 TTGGCTTAA GGCCCTTTT TATCAGAG TCCCTCTGCTG TGAGATTGCT TGCCCTGCTG CTGATGTGAC CAGTGGCAGG CACAGTCCA GGGAGACAGA CTTGAAATGG GACTGAGTCC
 CAGAAACAG TCTTTTCCGA TGAGACTTCAG CCACCATTT CAGCTCTGCA AGCTCTGGA CTCTCTAAG CACTCTCAG GAGAGCACA GTGCCACTG CTTCTCAAA
 TCACATTGT GCTGCTGAC TTCTGTGCC TGGACAGTT GAGAGCTGA CTGGCAAGA AGAGGAGG AGAGGAGG AGTTGAGGAG GTGAGGCTG TTGACTGTT
 AGATTAAAT GTATTATGAT GAGATATAA GCAAACTGT GCCTAATAA AAAAAAAAA A (SEQ. ID NO.: 11)

FIGURE 1

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CGAGCTCG CGAGCTCG GATGTCGNA CGCGGAGG AGNAGATG CGCGGAGG CGAGAGAA TGCCAGCC CGGAGCCC TGATCGCA GGAGCCCC 120
 R A S A E L G S A K G H R T R K E G R H P R A P R E N A T A R E P L D R Q E P P
 CGAGGCGC AGAGGAGC CGAGGCGC CGGACAGC AGCTGAGC CGGAGGCT CGGAGGCT GATGATGC TGTCAATCTA CAGGACTTAC 240
 P R P Q E F P Q R P P Q Q P E A R E P P G R G P R L V P H E Y H L S I Y R T Y
 TCGATCGCG AGAGCTGG CATCAATGCT AGCTTTTCC AGCTTTTCA AGCTTTTCA GTCTTTTCA GTCTTTTCA GTCTTTTCA GTCTTTTCA GTCTTTTCA 360
 S I A E K L G I N A S F F Q S S K S A N T I T S F V D R G L D D L S H T P L R R
 CAGAGTAT TGTGATGT GTGAGGCTC TCAGAGAG AGAGCTGT GGGGCGGAG GTGGGCTGT TTGCGGAGC CGCGGCGC CGCGGCGC TCCGTTGCA 480
 O K Y L F D V S T L S D K E E L V G A D V R L F R Q A P A L A P A A A P L A
 GCTCTGCC TCCAGTGC CCTGCTGT GGAAGCGG AGCTGACC CGAGGCGG CGCGGCGC GTGGGAGT CTTCGAGTG TGCGGCGC TCGCGGCGC CGCTGGAAG 600
 A L R L P V A P A A G S A E P G P A G A P R P G W E V F D V W R G L R P Q P W K
 CAGCTGCT TCGAGTTG GCGGCTGT GCGGCGAG GCGGCGAG GCGGCGAG GCGGCGAG GCGGCGAG GCGGCGAG GCGGCGAG GCGGCGAG 720
 Q I C L E L R A A W G G E P G A A E D E A R T P G P Q Q P P P D L R S L G F G
 CGAGGCTG GAGGCGCG TTGCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG 840
 R R V R T P Q E R A L L V V F S R S O R K T L F A E H R E Q L G S A T E V V G P
 GGTGCTGG CGAGGCTG GCGGCGCG CGCGGCGC CGCGGCGC CGCGGCGC CGCGGCGC CGCGGCGC CGCGGCGC CGCGGCGC CGCGGCGC 960
 G G A E G S G P P P P P P P P P P S G T P D A G L W S P S P G R R R T A F A
 AGCGGCGC GAGGCGCG GAGGCGCG GAGGCGCG GAGGCGCG GAGGCGCG GAGGCGCG GAGGCGCG GAGGCGCG GAGGCGCG GAGGCGCG 1080
 S R H G K R H G K K S R L R C S K K P L H V N F K E L G W D D W L L A P L E Y E
 GCTTACCT GCGAGGCT GTGAGCTC CGGCTGCT CGGAGCTG GCGGCGCG GCGGCGCG GCGGCGCG GCGGCGCG GCGGCGCG GCGGCGCG 1200
 A L H C E S V C D E P L R S H L E P T N H A L L Q T L M N S H D P G S T P P S C
 TCGGCGCG CCAATGAC TCCATGAC ATCTGTGTA TCGAGCGG CAAATGAT GTCTACAAG AGTACAGGA GATGCTGCT GCTGCGG 1308
 V P T K L T P I S I L Y I D A G N N V V Y N E Y E E M V V E S C G C R

FIGURE 2

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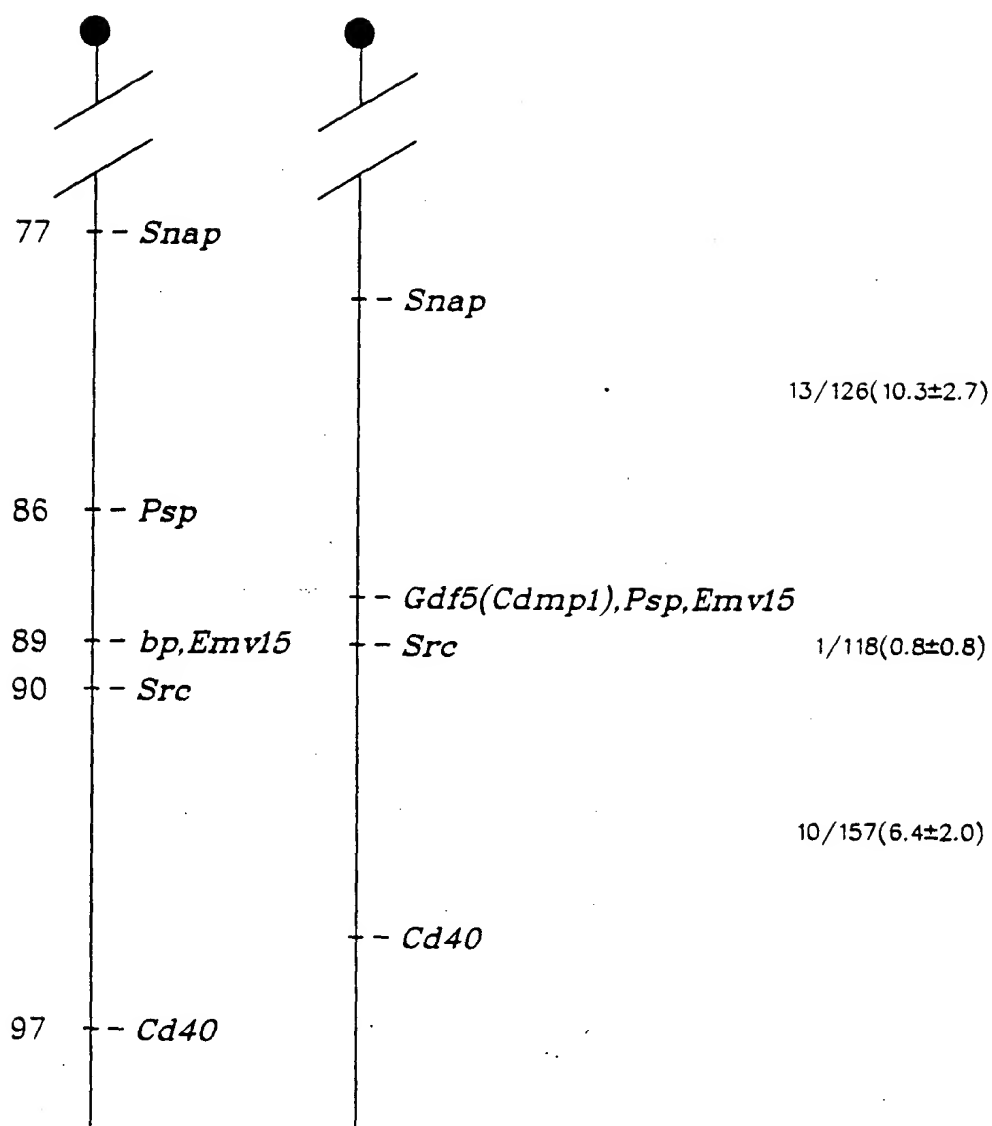


FIG. 3

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Xenopus CDMP-x	WI	I	APL	E	YEA	H	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:16)
Human CDMP-1	WI	I	APL	E	YEA	F	HCEG	D	C	E	FP	LRSHLEPTNH	A	(SEQ ID NO:17)
Chicken CDMP-x	WI	I	APL	E	YEA	Y	HCEG	D	C	E	FP	LRSHLEPTNH	A	(SEQ ID NO:18)
Zebrafish CDMP-3	WI	V	APL	D	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:19)
Xenopus CDMP-x	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:20)
Human CDMP-2	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:21)
Bovine CDMP-2	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:22)
Zebrafish CDMP-x	WI	M	APL	D	YEA	Y	HCEG	D	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:23)
Consensus	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:24)

FIGURE 4

See substitute figures 4 files 12/11/200 (open no. 4)
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